

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/731,632

Source: IFW/16

Date Processed by STIC: 2/16/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 02/16/2005

PATENT APPLICATION: US/09/731,632

TIME: 15:23:47

Input Set : N:\Crf3\RULE60\09731632.raw

Output Set: N:\CRF4\02162005\I731632.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Kennedy, Brian P.

6 Cromlish, Wanda A.

7 Mancini, Joseph A.

8 O'Neil, Gary

9 Vickers, Philip J.

10 Wong, Elizabeth

12 (ii) TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 cDNA AND

13 ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY

15 (iii) NUMBER OF SEQUENCES: 14

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Merck & Co., Inc.

19 (B) STREET: 126 Lincoln Avenue

20 (C) CITY: Rahway

21 (D) STATE: NJ

22 (E) COUNTRY: USA

23 (F) ZIP: 07065

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Diskette, 3.5 in, 1.4kb

27 (B) COMPUTER: Apple Macintosh

28 (C) OPERATING SYSTEM: System 7

29 (D) SOFTWARE: Microsoft Word 5

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/731,632

C--> 33 (B) FILING DATE: 20-Nov-2000

34 (C) CLASSIFICATION: 435

36 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/08/064,271

38 (B) FILING DATE: 06-MAY-1993

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Panzer, Curtis C.

42 (B) REGISTRATION NUMBER: 33,752

43 (C) REFERENCE/DOCKET NUMBER: 18906IA

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: (908)594-3199

47 (B) TELEFAX: (908)594-4720

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 24 bases

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

56 (D) TOPOLOGY: linear

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58      (ii) MOLECULE TYPE: DNA (genomic)
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 TGCCCAGCTC CTGGCCCGCC GCTT
66 (2) INFORMATION FOR SEQ ID NO: 2:
68      (i) SEQUENCE CHARACTERISTICS:
69          (A) LENGTH: 24 bases
70          (B) TYPE: nucleic acid
71          (C) STRANDEDNESS: single
72          (D) TOPOLOGY: linear
74      (ii) MOLECULE TYPE: DNA (genomic)
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
80 GTGCATCAAC ACAGGCGCCT CTTC
82 (2) INFORMATION FOR SEQ ID NO: 3:
84      (i) SEQUENCE CHARACTERISTICS:
85          (A) LENGTH: 27 bases
86          (B) TYPE: nucleic acid
87          (C) STRANDEDNESS: single
88          (D) TOPOLOGY: linear
90      (ii) MOLECULE TYPE: DNA (genomic)
94      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
96 TTCAAATGAG ATTGTGGGAA AATTGCT
98 (2) INFORMATION FOR SEQ ID NO: 4:
100     (i) SEQUENCE CHARACTERISTICS:
101         (A) LENGTH: 24 bases
102         (B) TYPE: nucleic acid
103         (C) STRANDEDNESS: single
104         (D) TOPOLOGY: linear
106     (ii) MOLECULE TYPE: DNA (genomic)
110     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
112 AGATCATCTC TGCCTGAGTA TCTT
114 (2) INFORMATION FOR SEQ ID NO: 5:
116     (i) SEQUENCE CHARACTERISTICS:
117         (A) LENGTH: 24 bases
118         (B) TYPE: nucleic acid
119         (C) STRANDEDNESS: single
120         (D) TOPOLOGY: linear
122     (ii) MOLECULE TYPE: DNA (genomic)
126     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
128 CCACCCATGG CAAATTCCAT GGCA
130 (2) INFORMATION FOR SEQ ID NO: 6:
132     (i) SEQUENCE CHARACTERISTICS:
133         (A) LENGTH: 24 bases
134         (B) TYPE: nucleic acid
135         (C) STRANDEDNESS: single
136         (D) TOPOLOGY: linear
138     (ii) MOLECULE TYPE: DNA (genomic)
142     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
144 TCTAGACGGC AGGTCAGGTC CACC
146 (2) INFORMATION FOR SEQ ID NO: 7:

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148      (i) SEQUENCE CHARACTERISTICS:
149          (A) LENGTH: 12 amino acids
150          (B) TYPE: amino acid
151          (C) STRANDEDNESS: single
152          (D) TOPOLOGY: linear
154      (ii) MOLECULE TYPE: protein
158      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
160      Asp Asp Ile Asn Pro Thr Val Leu Leu Lys Glu Arg
161      1          5          10
162  (2) INFORMATION FOR SEQ ID NO: 8:
164      (i) SEQUENCE CHARACTERISTICS:
165          (A) LENGTH: 23 bases
166          (B) TYPE: nucleic acid
167          (C) STRANDEDNESS: single
168          (D) TOPOLOGY: linear
170      (ii) MOLECULE TYPE: DNA (genomic)
174      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
176  CTGCGATGCT CGCCGCGCC CTG
178  (2) INFORMATION FOR SEQ ID NO: 9:
180      (i) SEQUENCE CHARACTERISTICS:
181          (A) LENGTH: 24 bases
182          (B) TYPE: nucleic acid
183          (C) STRANDEDNESS: single
184          (D) TOPOLOGY: linear
186      (ii) MOLECULE TYPE: DNA (genomic)
190      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
192  CTTCTACAGT TCAATCGAAC GTTC
194  (2) INFORMATION FOR SEQ ID NO: 10:
196      (i) SEQUENCE CHARACTERISTICS:
197          (A) LENGTH: 604 amino acids
198          (B) TYPE: amino acid
199          (C) STRANDEDNESS: single
200          (D) TOPOLOGY: linear
202      (ii) MOLECULE TYPE: protein
206      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
208      Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
209      1          5          10          15
211      Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
212      20          25          30
214      Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
215      35          40          45
217      Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
218      50          55          60
220      Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
221      65          70          75          80
223      Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
224      85          90          95
226      Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
227      100          105          110

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229   Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
230           115                      120                      125
232   Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
233           130                      135                      140
235   Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser
236           145                      150                      155                      160
238   Asn Glu Ile Val Glu Lys Leu Leu Leu Arg Arg Lys Phe Ile Pro Asp
239           165                      170                      175
241   Pro Gln Gly Ser Asn Met Met Phe Ala Phe Phe Ala Gln His Phe Thr
242           180                      185                      190
244   His Gln Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn
245           195                      200                      205
247   Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Glu Thr Leu
248           210                      215                      220
250   Ala Arg Gln Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr
251           225                      230                      235                      240
253   Gln Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Gln
254           245                      250                      255
256   Ala Glu Met Ile Tyr Pro Pro Gln Val Pro Glu His Leu Arg Phe Ala
257           260                      265                      270
259   Val Gly Gln Glu Val Phe Gly Leu Val Pro Gly Leu Met Tyr Ala
260           275                      280                      285
262   Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Gln
263           290                      295                      300
265   Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu
266           305                      310                      315                      320
268   Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln
269           325                      330                      335
271   His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu
272           340                      345                      350
274   Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn
275           355                      360                      365
277   Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His
278           370                      375                      380
280   Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu
281           385                      390                      395                      400
283   Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
284           405                      410                      415
286   Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
287           420                      425                      430
289   Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
290           435                      440                      445
292   Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe
293           450                      455                      460
295   Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
296           465                      470                      475                      480
298   Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
299           485                      490                      495
301   Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly

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302          500          505          510
304      Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
305          515          520          525
307      Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
308          530          535          540
310      Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
311          545          550          555          560
313      Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
314          565          570          575
316      Val Thr Ile Asn Ala Ser Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
317          580          585          590
319      Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu
320          595          600
322 (2) INFORMATION FOR SEQ ID NO: 11:
324     (i) SEQUENCE CHARACTERISTICS:
325         (A) LENGTH: 3387 bases
326         (B) TYPE: nucleic acid
327         (C) STRANDEDNESS: single
328         (D) TOPOLOGY: linear
330     (ii) MOLECULE TYPE: DNA (genomic)
334     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
336 GTCCAGGAAC TCCTCAGCAG CGCCTCCTTC AGCTCCACAG CCAGACGCCC TCAGACAGCA      60
338 AAGCCTACCC CCGCGCCGCG CCCTGCCCCG CGCTGCGATG CTCGCCCCGCG CCCTGCTGCT      120
340 GTGCGCGGTC CTGGCGCTCA GCCATACAGC AAATCCTTGC TGTTCCCAACC CATGTCAAAA      180
342 CCGAGGTGTA TGTATGAGTG TGGGATTTGA CCAGTATAAG TGCGATTGTA CCCGGACAGG      240
344 ATTCTATGGA GAAACTGCT CAACACCGGA ATTTTGTACA AGAATAAAAT TATTTCTGAA      300
346 ACCCACTCCA AACACAGTGC ACTACATACT TACCACTTTC AAGGGATTTT GGAACGTTGT      360
348 GAATAACATT CCCTTCCTTC GAAATGCAAT TATGAGTTAT GTGTTGACAT CCAGATCACA      420
350 TTTGATTGAC AGTCCACCAA CTTACAATGC TGACTATGGC TACAAAAGCT GGAAGCCTT      480
352 CTCTAACCTC TCCTATTATA CTAGAGCCCT TCCTCCTGTG CCTGATGATT GCCCGACTCC      540
354 CTTGGGTGTC AAAGGTAAAA AGCAGCTTCC TGATTCAAAT GAGATTGTGG AAAAATTGCT      600
356 TCTAAGAAGA AAGTTCATCC CTGATCCCCA GGGCTCAAAC ATGATGTTTG CATTCTTTGC      660
358 CCAGCACTTC ACGCACCAGT TTTTCAAGAC AGATCATAAG CGAGGGCCAG CTTTCACCAA      720
360 CGGGCTGGGC CATGGGGTGG ACTTAAATCA TATTACGGT GAAACTCTGG CTAGACAGCG      780
362 TAAACTGCGC CTTTTC AAGG ATGGAAAAAT GAAATATCAG ATAATTGATG GAGAGATGTA      840
364 TCCTCCCA CA GTCAAAGATA CTCAGGCAGA GATGATCTAC CCTCCTCAAG TCCCTGAGCA      900
366 TCTACGGTTT GCTGTGGGGC AGGAGGTCTT TGGTCTGGTG CCTGGTCTGA TGATGTATGC      960
368 CACAATCTGG CTGCGGGAAC ACAACAGAGT ATGTGATGTG CTTAAACAGG AGCATCCTGA      1020
370 ATGGGGTGAT GAGCAGTTGT TCCAGACAAG CAGGCTAATA CTGATAGGAG AGACTATTAA      1080
372 GATTGTGATT GAAGATTATG TGCAACACTT GAGTGGCTAT CACTTCAAAC TGAAATTTGA      1140
374 CCCAGAACTA CTTTTC AACA AACAATTCCA GTACCAAAAAT CGTATTGCTG CTGAATTTAA      1200
376 CACCCTCTAT CACTGGCATC CCCTTCTGCC TGACACCTTT CAAATTCATG ACCAGAAATA      1260
378 CAACTATCAA CAGTTTATCT ACAACAATC TATATTGCTG GAACATGGAA TTACCCAGTT      1320
380 TGTTGAATCA TTCACCAGGC AAATTGCTGG CAGGGTTGCT GGTGGTAGGA ATGTTCCACC      1380
382 CGCAGTACAG AAAGTATCAC AGGCTTCCAT TGACCAGAGC AGGCAGATGA AATACCAGTC      1440
384 TTTTAATGAG TACCGCAAAC GCTTTATGCT GAAGCCCTAT GAATCATTTG AAGAACTTAC      1500
386 AGGAGAAAAG GAAATGTCTG CAGAGTTGGA AGCACTCTAT GGTGACATCG ATGCTGTGGA      1560
388 GCTGTATCCT GCCCTTCTGG TAGAAAAGCC TCGGCCAGAT GCCATCTTTG GTGAAACCAT      1620
390 GGTAGAAGTT GGAGACCAT TCTCCTTGAA AGGACTTATG GGTAATGTTA TATGTTCTCC      1680

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/731,632

DATE: 02/16/2005
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Input Set : N:\Crf3\RULE60\09731632.raw
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 66
Seq#:2; Line(s) 82
Seq#:3; Line(s) 98
Seq#:4; Line(s) 114
Seq#:5; Line(s) 130
Seq#:6; Line(s) 146
Seq#:7; Line(s) 162
Seq#:8; Line(s) 178
Seq#:9; Line(s) 194
Seq#:10; Line(s) 322
Seq#:11; Line(s) 451
Seq#:12; Line(s) 467
Seq#:13; Line(s) 483

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/731,632

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Input Set : N:\Crf3\RULE60\09731632.raw

Output Set: N:\CRF4\02162005\I731632.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]